

## SEQUENCE LISTING

5 <110> SunGene GmbH & Co. KGaA

10 <120> Process for the preparation of  $\beta$ -carotenoids

<130> PF 54755

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20 <170> PatentIn version 3.1

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 5 <211> 309  
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 20 Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys Pro Thr Ser Thr Thr  
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 35 40 45  
 25 Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu  
 50 55 60  
 30 Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu  
 65 70 75 80  
 35 Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu  
 85 90 95  
 40 Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met  
 100 105 110  
 Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met Ala Val Tyr Tyr Arg  
 115 120 125  
 45 Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu  
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 50 Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp  
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<221> CDS

&lt;222&gt; (141) .. (1691)

&lt;223&gt;

5

&lt;400&gt; 7

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10 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120

agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173

Met Ser Met Arg Ala Gly His Met Thr Ala Thr

1 5 10

15

atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221

Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr

15 20 25

20 aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269

Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln

30 35 40

gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg 317

25 Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu

45 50 55

ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc 365

Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser

30 60 65 70 75

cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt 413

Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser

80 85 90

35

aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt 461

Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu

95 100 105

40 gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc 509

Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile

110 115 120

ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa 557

45 Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu

125 130 135

ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat 605

Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp

50 140 145 150 155

act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc 653

Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala

160 165 170

	tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701
	Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
	175 180 185	
5	tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
	Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
	190 195 200	
10	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797
	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
	205 210 215	
15	aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
	Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
	220 225 230 235	
20	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
	Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
	240 245 250	
25	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
	Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
	255 260 265	
30	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
	Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
	270 275 280	
35	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
	Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
	285 290 295	
40	cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
	Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
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45	atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act	1133
	Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	
	320 325 330	
50	atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att	1181
	Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
	335 340 345	
55	cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
	Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
	350 355 360	
60	ggg gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
	Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
	365 370 375	
65	aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325



## 17

	Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile	
	380 385 390 395	
5	tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr	1373
	400 405 410	
10	acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg	1421
	415 420 425	
15	aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln	1469
	430 435 440	
	atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu	1517
	445 450 455	
20	ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr	1565
	460 465 470 475	
25	gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser	1613
	480 485 490	
30	ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly	1661
	495 500 505	
35	aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag Thr Met Leu Lys Ala Tyr Leu Thr Ile	1711
	510 515	
	tttagattat aggcacatct tgcatatata tatgtataaaa ccttatgtgt gctgtatcct	1771
	tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg	1830
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	<211> 516	
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50	<400> 8	
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	Cys	Pro	Arg	Phe	Met	Thr	Ser	Ile	Arg	Tyr	Thr	Lys	Gln	Ile	Lys	Cys	
				20					25					30			
5																	
	Asn	Ala	Ala	Lys	Ser	Gln	Leu	Val	Val	Lys	Gln	Glu	Ile	Glu	Glu	Glu	
			35					40					45				
10																	
	Glu	Asp	Tyr	Val	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	Met	
		50					55					60					
15																	
	Gln	Gln	Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	Leu	Ser	Gln	Lys	Leu	
	65					70					75					80	
20																	
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25																	
	Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Gly	Glu	
				100					105					110			
30																	
	Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Ala	Leu	Ile	Gly	Pro	Asp	Leu	Pro	
			115					120					125				
35																	
	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Ile	Gly	Leu	Gly	
		130					135					140					
40																	
	Leu	Glu	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Val	Val	Tyr	Leu	
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45																	
	Asp	Asp	Asn	Asp	Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	
					165					170					175		
50																	
	Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Thr	Arg	Cys	Met	Glu	Ser	Gly	
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55																	
	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Pro	Asn	
			195					200					205				
60																	
	Gly	Leu	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	Thr	Ile	Pro	Cys	Arg	
		210					215					220					

	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr	
	225					230					235					240	
5	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Ile	Glu	
					245					250					255		
10	Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	
				260					265					270			
15	Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	His	Lys	Ser	Gln	Ser	Leu	Glu	Ala	Gln	
			275					280					285				
20	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Lys	Val	Phe	
		290					295					300					
25	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Glu	Ala	Met	Pro	Phe	Glu	Leu	
	305					310					315					320	
30	Leu	Lys	Thr	Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	Met	Gly	Ile	Arg	Ile	
					325					330					335		
35	Thr	Lys	Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	
				340					345					350			
40	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	
			355					360					365				
45	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	
		370					375					380					
50	Ala	Pro	Asn	Tyr	Ala	Ala	Val	Ile	Ala	Lys	Ile	Leu	Gly	Lys	Gly	Asn	
	385					390					395					400	
55	Ser	Lys	Gln	Met	Leu	Asp	His	Gly	Arg	Tyr	Thr	Thr	Asn	Ile	Ser	Lys	
					405					410					415		
60	Gln	Ala	Trp	Glu	Thr	Leu	Trp	Pro	Leu	Glu	Arg	Lys	Arg	Gln	Arg	Ala	
				420					425					430			
65	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	Ile	Val	Gln	Met	Asp	Ile	Glu	Gly	
			435					440					445				

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp  
 450 455 460  
 5

Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe  
 465 470 475 480  
 10

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu  
 485 490 495  
 15

Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala  
 500 505 510  
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Tyr Leu Thr Ile  
 515

<210> 9

25 <211> 358

<212> DNA

30 <213> Tagetes erecta

<220>

35 <221> Sense promoter

<222> (1)..(358)

40 <223>

<400> 9

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 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180  
 50 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240  
 aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300  
 tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtg tttgttgttg ttgtcgac 358

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 5 <211> 445  
 <212> DNA  
 10 <213> *Tagetes erecta*  
 <220>  
 15 <221> Sense fragment  
 <222> (1)..(445)  
 20 <223>  
 <400> 10  
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 gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180  
 30 ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240  
 caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300  
 gaaagccggt ggatcggagc tgctttttgt tcaaatgcaa cagaataagt ccatggatgc 360  
 35 acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420  
 ctgtatactg gatttggttg tcgac 445  
 40 <210> 11  
 <211> 446  
 45 <212> DNA  
 <213> *Tagetes erecta*  
 50 <220>  
 <221> Antisense fragment

&lt;222&gt; (1)..(446)

&lt;223&gt;

5

&lt;400&gt; 11

gaattcgcac gaggcaaagc aaagggttggt tgttggttggt gttgagagac actccaatcc 60

10

aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

gaaaaagaat cattaactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

15

ggcggtttt acatgcccta gggttatgac tagcatcaga tacacgaagc aaattaagtg 240

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaagtcaa cagaataagt ccatggatgc 360

20

acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gatcct 446

25

&lt;210&gt; 12

&lt;211&gt; 393

&lt;212&gt; DNA

30

&lt;213&gt; Tagetes erecta

35

&lt;220&gt;

&lt;221&gt; Sense fragment

&lt;222&gt; (1)..(393)

40

&lt;223&gt;

45

&lt;400&gt; 12

aagcttttga ttagcactga ttgtccagat ggatattgag gggaccgcga cattcttccg 60

gactttcttc cgcttgccca catggatgtg gtggggggtt cttggatctt cgttatcatc 120

50

aactgacttg ataatatttg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

gggtctggtt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata 300

tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct 360  
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 <211> 397  
 10 <212> DNA  
 <213> Tagetes erecta  
 15  
 <220>  
 <221> Antisense fragment  
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 <223>  
 25  
 <400> 13  
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 catcaactga cttgataata tttgcgtttt acatgtttat catagcaccg catagcctga 180  
 gaatgggtct ggttagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt 240  
 35 atctcagat ataaataact ctagtgcgga tcagtttaga ttataggcac atcttgcata 300  
 tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat 360  
 40 ttcttggggg aatgctgatg aagtattttc tggatcc 397  
 <210> 14  
 45 <211> 358  
 <212> DNA  
 <213> Tagetes erecta  
 50  
 <220>

&lt;221&gt; Sense promoter

&lt;222&gt; (1)..(358)

5 &lt;223&gt;

&lt;400&gt; 14

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 gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120  
 15 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180  
 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240  
 aagatggctt ggctgctaata caactcaact caactcatat cctatccatt caaattcaat 300  
 20 tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtt tttgttgttg ttgtcgac 358

&lt;210&gt; 15

25 &lt;211&gt; 361

&lt;212&gt; DNA

30 &lt;213&gt; Tagetes erecta

&lt;220&gt;

35 &lt;221&gt; Antisense promoter

&lt;222&gt; (1)..(361)

40 &lt;223&gt;

&lt;400&gt; 15

45 ctcgagctta ccgatagtaa aatcgtagt tatgattaat acttgggagg tgggggatta 60  
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgagggt 120  
 aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180  
 50 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240  
 taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300  
 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttggatc 360



c

361

5 <210> 16  
 <211> 332  
 <212> DNA  
 10 <213> *Tagetes erecta*

15 <220>  
 <221> CDS  
 <222> (1)..(330)  
 20 <223>

25 <400> 16  
 aag ctt gca cga gcc tct ctc tat ttt tac act tca atg gcg gca gca 48  
 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala  
 1 5 10 15

30 att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96  
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg  
 20 25 30

35 tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144  
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45

40 ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192  
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60

45 gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240  
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80

agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288  
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val  
 85 90 95

50 atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac 332  
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 100 105 110

<210> 17  
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 5 <212> PRT  
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 10  
 <400> 17  
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 1 5 10 15  
 15 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg  
 20 20 25 30  
 20 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45  
 25 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60  
 30 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80  
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val  
 85 90 95  
 35 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser  
 100 105 110  
 40  
 <210> 18  
 <211> 332  
 45 <212> DNA  
 <213> Tagetes erceta  
 50  
 <220>  
 <221> misc\_feature

&lt;222&gt; (1)..(332)

<223>  $\beta$ -Hydroxylase sense fragment

5

&lt;400&gt; 18

aagcttgac gagcctctct ctattttttac acttcaatgg cggcagcaat tgctgtccct 60

10

tgtagctcaa gaccatttgg cttaggtcga atgcgggttac ttggtcataa acccacaacc 120

ataacttgtc acttcccctt ttctttttct atcaaatcat ttacccaat tgtaggggc 180

15

agaagatgta ctgtttgttt tggtgccggg ggcgacagta atagtaacag taataataat 240

agtgcagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300

cgtttggttg aagaaaaaat ggagaggctg ac 332

20

&lt;210&gt; 19

&lt;211&gt; 332

25

&lt;212&gt; DNA

<213> *Tagetes erecta*

30

&lt;220&gt;

&lt;221&gt; misc\_feature

35

&lt;222&gt; (1)..(332)

<223>  $\beta$ -Hydroxylase antisense fragment

40

&lt;400&gt; 19

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ttgtagctca agaccatttg gcttaggtcg aatgcgggta ttggtcata aaccacaac 120

45

cataacttgt cacttcccct ttcttttttc tatcaaatca ttaccccaa ttgtagggg 180

cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

50

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	cggattccac caccacttg aaaaattgac atgtcacaat gatttcgtat cctagtcttt	180
25	tattatttaa cactctcaca atcccattac tctacacctc tttcattaag tcaacacacg	240
	gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct	300
	cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt	360
30	ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag	420
	ttcctcctct atatatttca aaagaatgga acagaaacat aaacgaaaga cagagtacct	480
35	gatgttgatg attcattgtc tgtctggagc tcccaaatgc cttttatgct tacatattca	540
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	aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg	660
40	gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagttgg aaacacctaca	720
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	cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga	960
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